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SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Method for the purification of an N-terminal fragment of hepatocyte growth factor

<130> 22389 WO

<150> EP 04004950.4

<151> 2004-03-03

<160> 2

<170> PatentIn version 3.2

<210> 1

<211> 1350

<212> DNA

<213> Artificial

<220>

<223> dna coding for NK4

<220>

<221> CDS

<222> (1)..(1350)

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atg tct cgt aaa cgt cgt aat act att cat gaa ttc aaa aaa tca gca  
Met Ser Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala  
1 5 10 15

48

aag act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa  
Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys  
20 25 30

96

aaa gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa  
Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys  
35 40 45

144

gga ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa  
Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys  
50 55 60

192

caa tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa  
Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Gly Val Lys Lys  
65 70 75 80

240

gaa ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga  
Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg  
85 90 95

288

aac tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc  
Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile  
100 105 110

336

- 2 -

act aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac	384
Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His	
115 120 125	
gaa cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa	432
Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu	
130 135 140	
aac tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc	480
Asn Tyr Cys Arg Asn Pro Arg Gly Glu Gly Pro Trp Cys Phe	
145 150 155 160	
aca agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt	528
Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys	
165 170 175	
tca gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt ctc	576
Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu	
180 185 190	
atg gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat cag	624
Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln	
195 200 205	
aca cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag ggc	672
Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly	
210 215 220	
ttt gat gat aat tat tgc cgc aat ccc gat ggc cag ccg agg cca tgg	720
Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp	
225 230 235 240	
tgc tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa	768
Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys	
245 250 255	
aca tgc gct gac aat act atg aat gac act gat gtt cct ttg gaa aca	816
Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr	
260 265 270	
act gaa tgc atccaa ggt caa gga gaa ggc tac agg ggc act gtc aat	864
Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn	
275 280 285	
acc att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat cct	912
Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro	
290 295 300	
cac gag cat gac atg act cct gaa aat ttc aag tgc aag gac cta cga	960
His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg	
305 310 315 320	
gaa aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt ttt	1008
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe	
325 330 335	

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acc act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca aac		1056	
Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn			
340	345	350	
tgt gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa aat		1104	
Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn			
355	360	365	
tat atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg		1152	
Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met			
370	375	380	
tgg gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa cca		1200	
Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro			
385	390	395	400
gat gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat		1248	
Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp			
405	410	415	
gct cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat		1296	
Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp			
420	425	430	
tat tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca atc gtt		1344	
Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val			
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taa tag		1350	

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<212> PRT  
<213> Artificial

<220>  
<223> protein-sequence of NK4

<400> 2

Met Ser Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala  
1 5 10 15

Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys  
20 25 30

Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys  
35 40 45

Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys  
50 55 60

- 4 -

Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys  
65 70 75 80

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg  
85 90 95

Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile  
100 105 110

Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His  
115 120 125

Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu  
130 135 140

Asn Tyr Cys Arg Asn Pro Arg Gly Glu Gly Gly Pro Trp Cys Phe  
145 150 155 160

Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys  
165 170 175

Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu  
180 185 190

Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln  
195 200 205

Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly  
210 215 220

Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp  
225 230 235 240

Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys  
245 250 255

Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr  
260 265 270

Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn  
275 280 285

Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro  
290 295 300

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His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg  
305 310 315 320

Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe  
325 330 335

Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn  
340 345 350

Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn  
355 360 365

Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met  
370 375 380

Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro  
385 390 395 400

Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp  
405 410 415

Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp  
420 425 430

Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val  
435 440 445